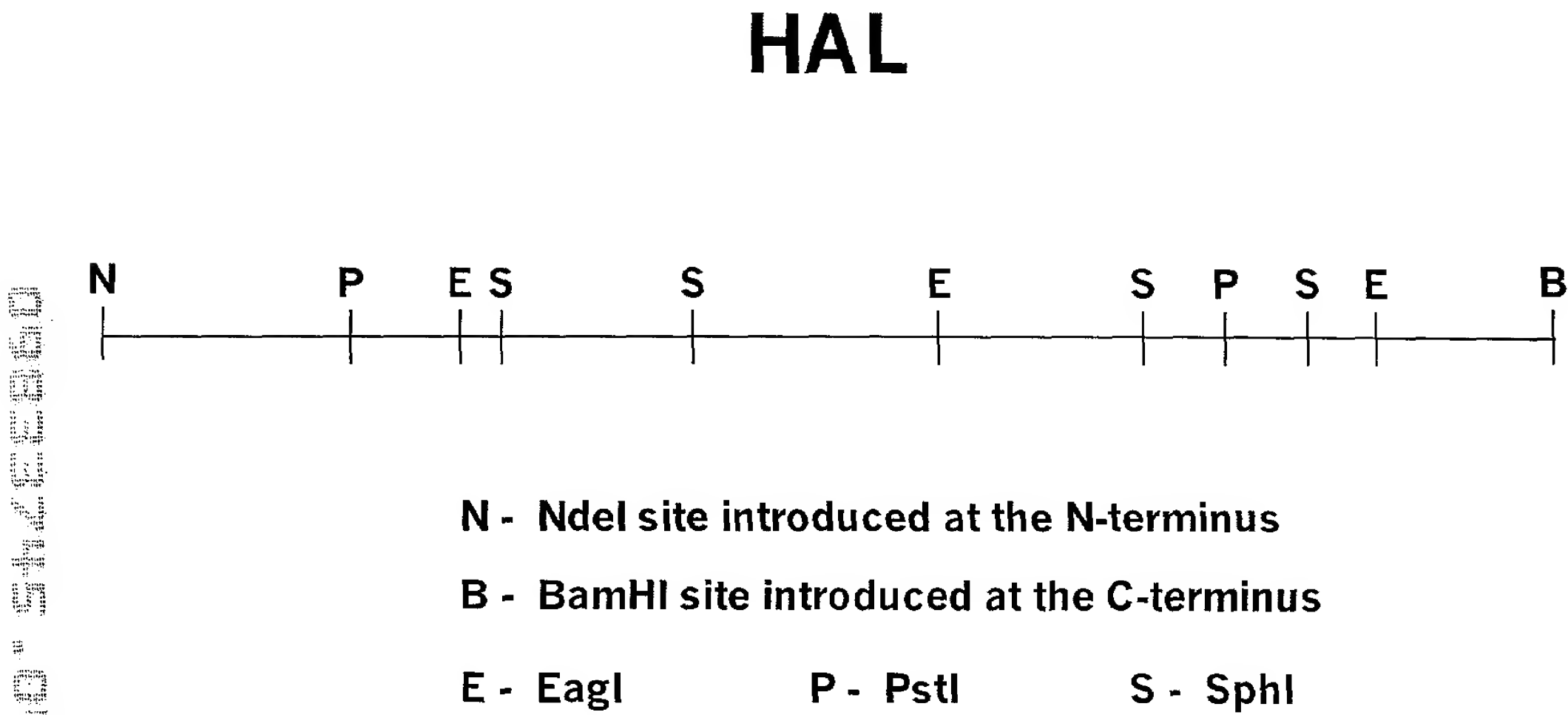


**Figure 1:** Restriction pattern of the HAL coding region cut with selected enzymes.



**Figure 2:** Experimentally derived peptide sequences of HAL

**Figure 3:** SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

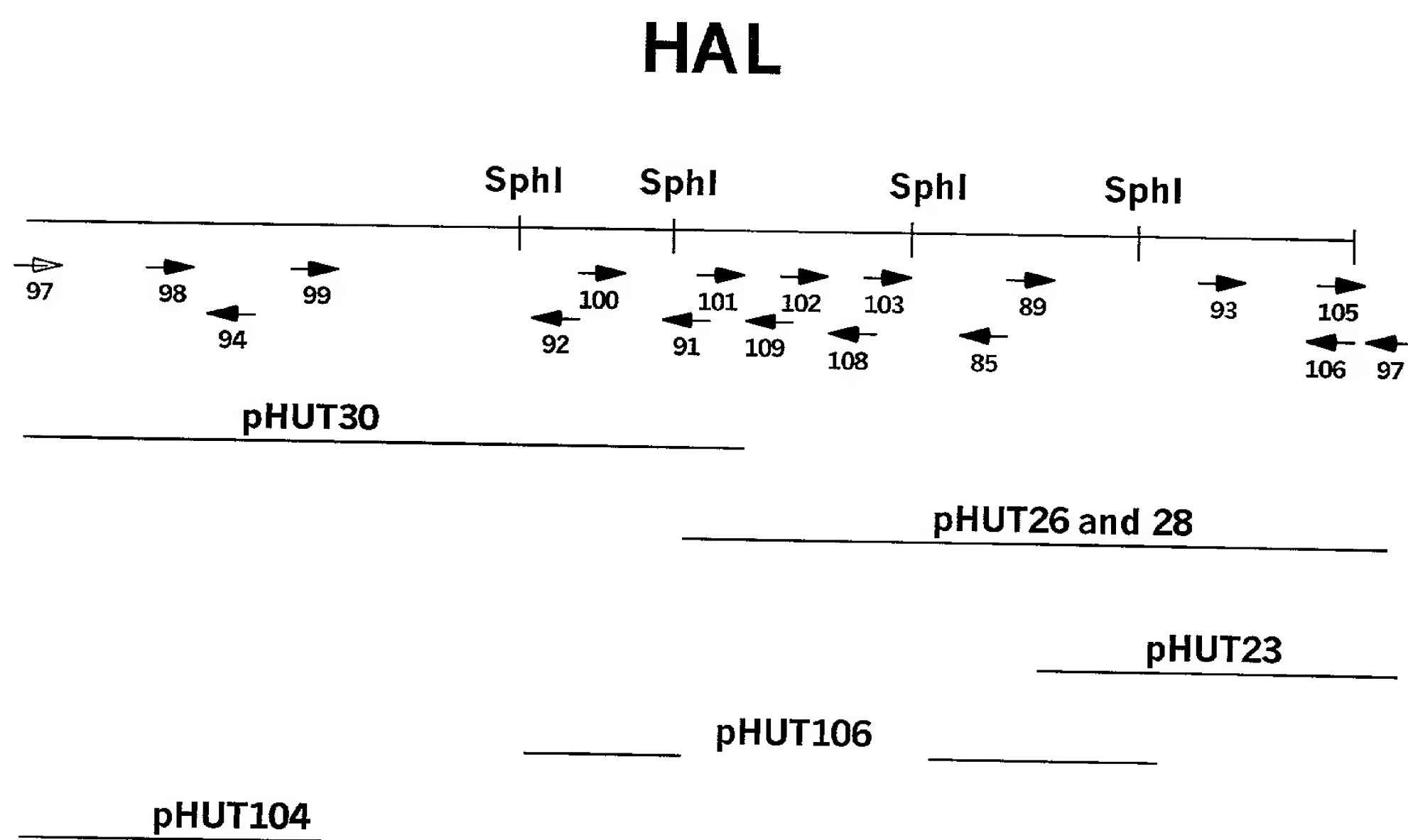
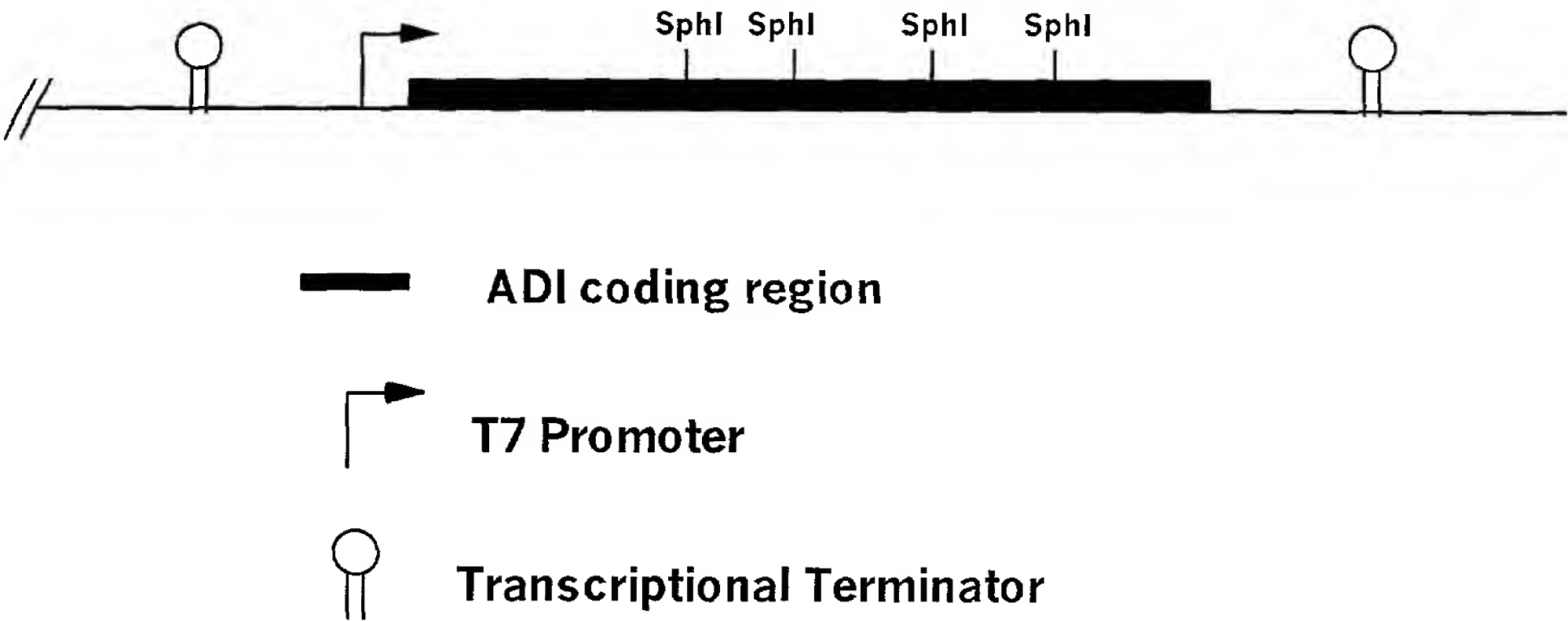
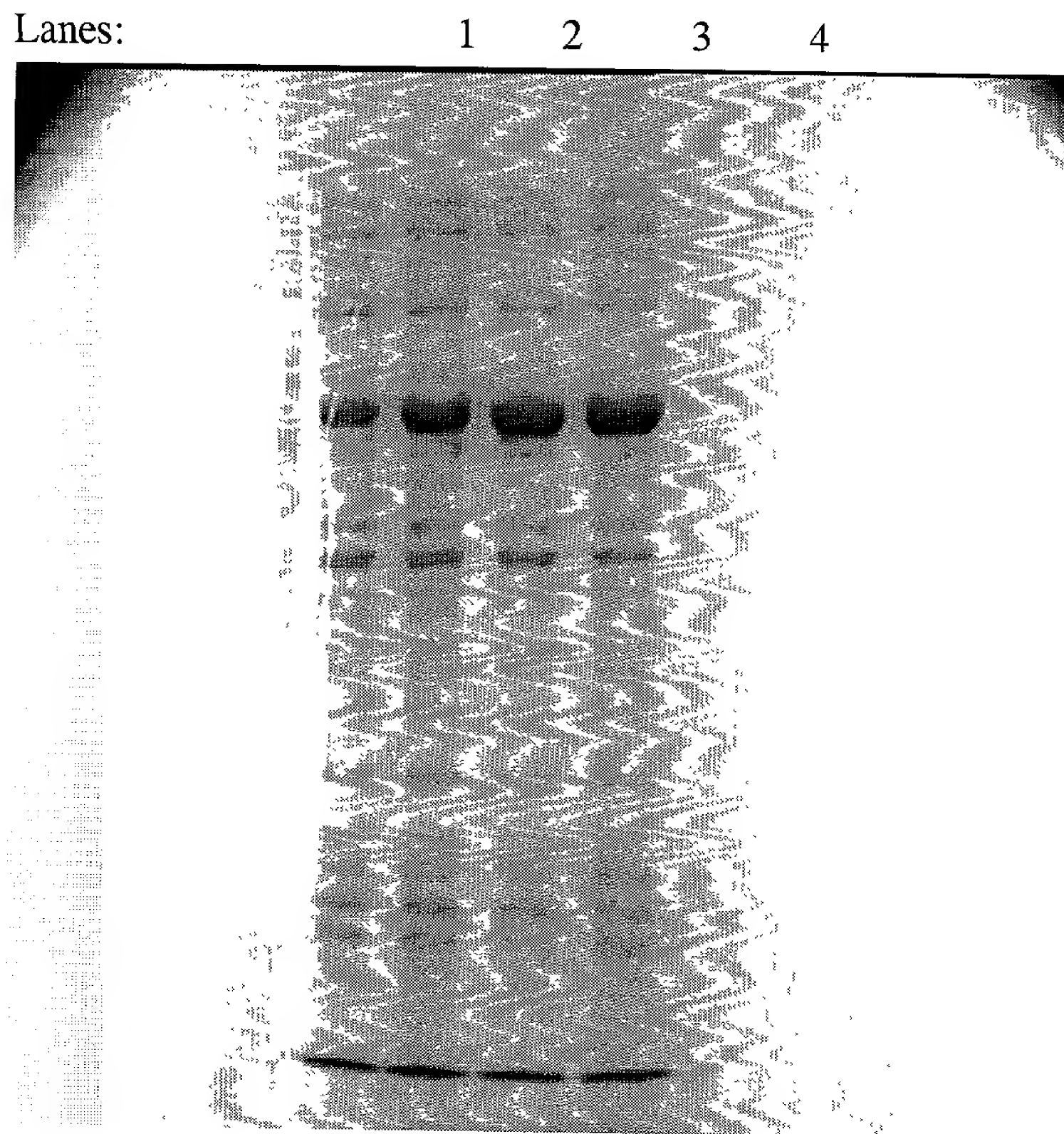


Figure 4: Histidine ammonia lyase overexpressing plasmid.

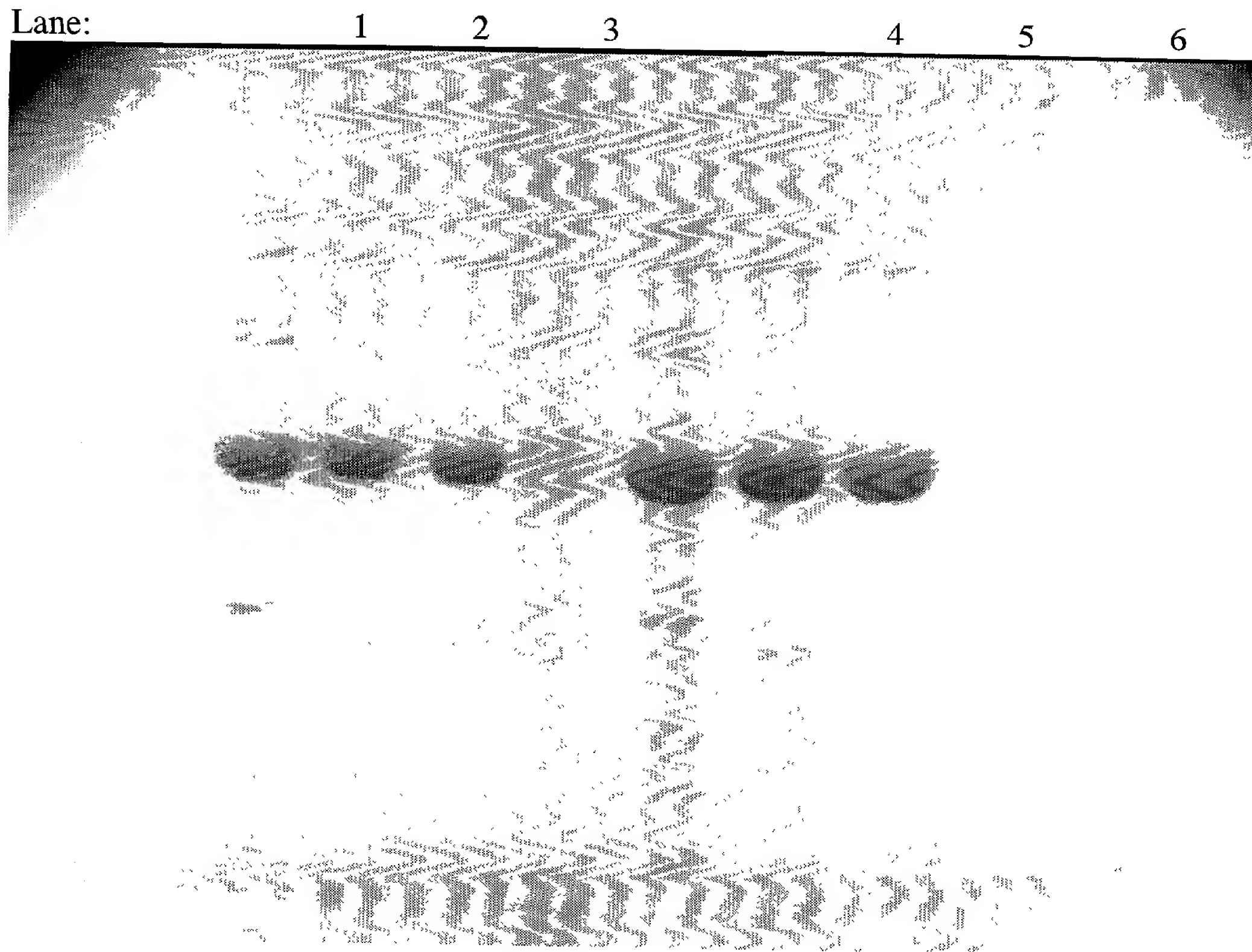
pHUT102



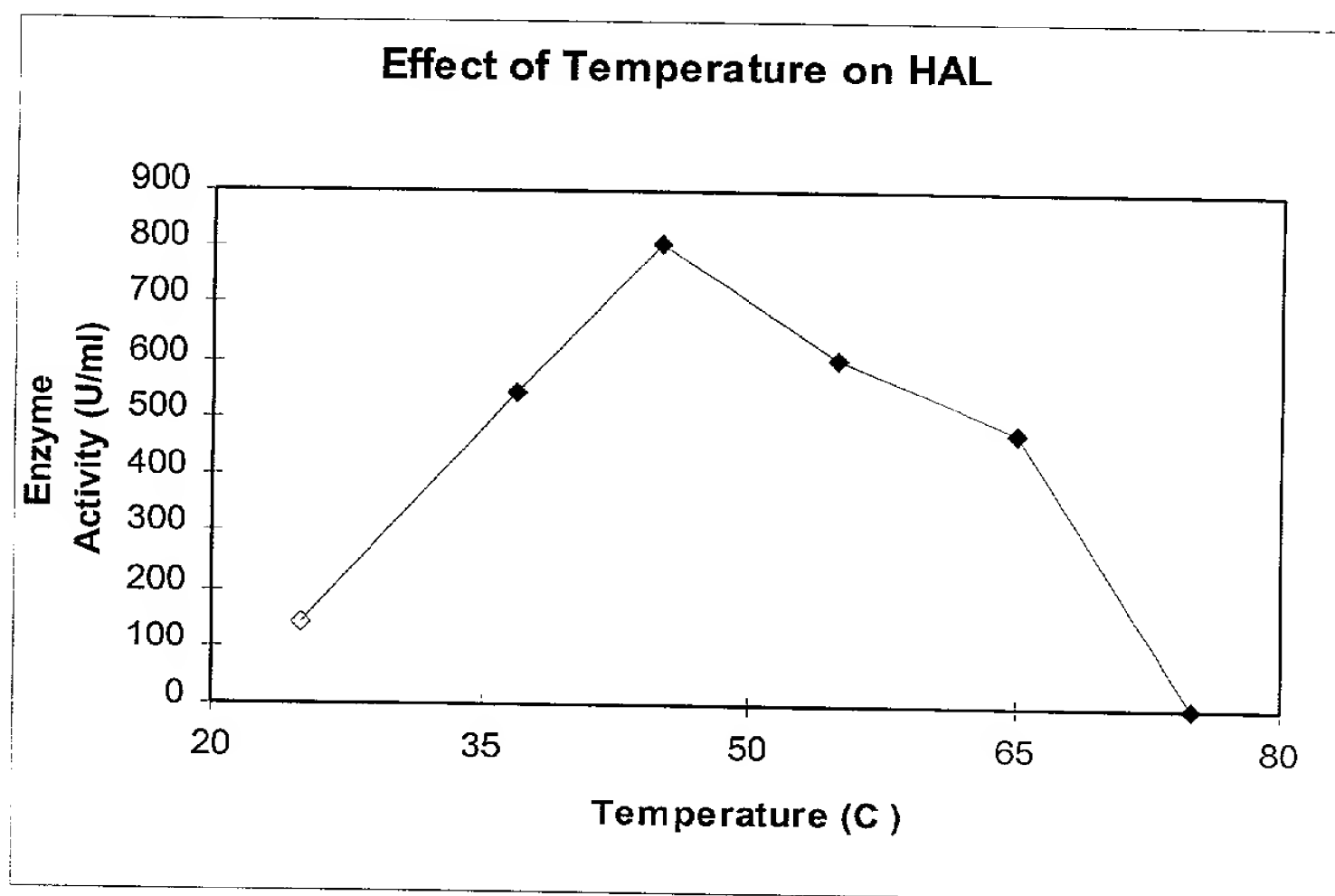
**Figure 5:** SDS-PAGE showing expression of HAL in *E. coli*.



**Figure 6:** SDS-PAGE showing purification of HAL from *E. coli*



**Figure 7: Effect of Temperature on HAL**



HAL and HAL

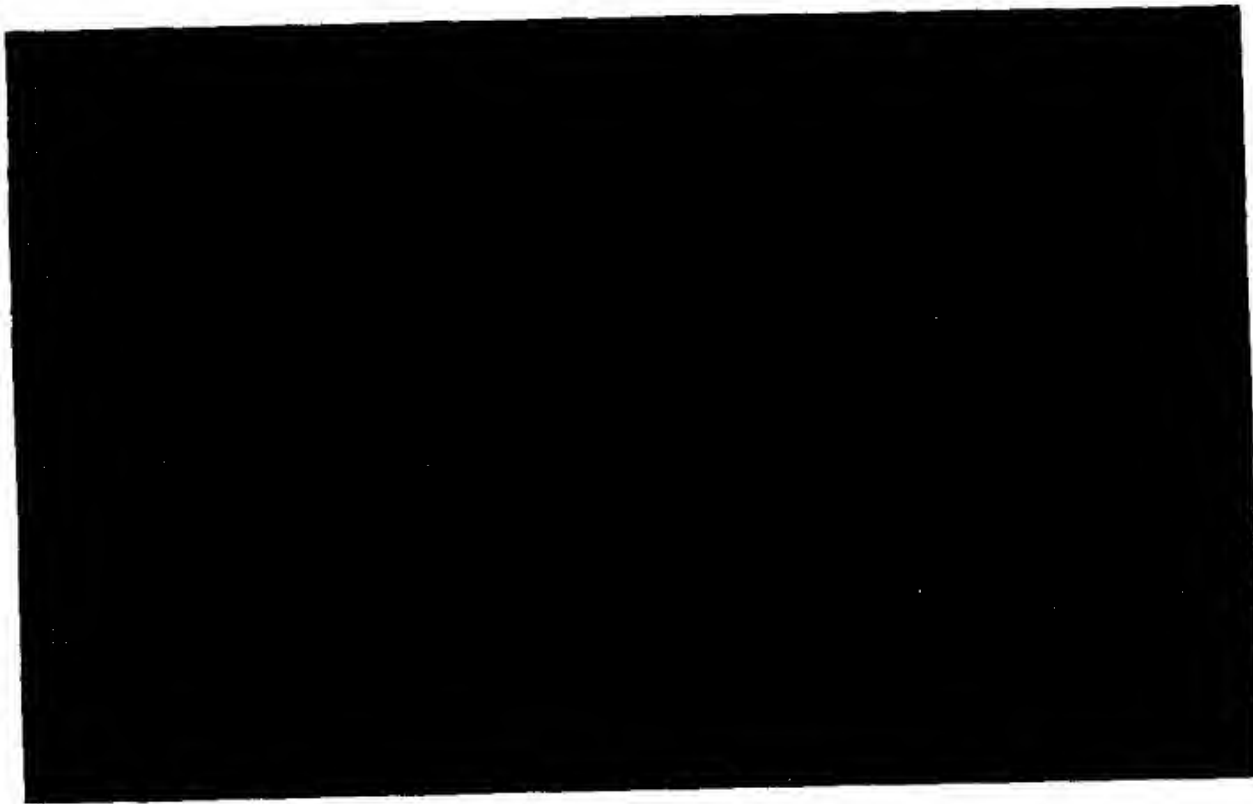
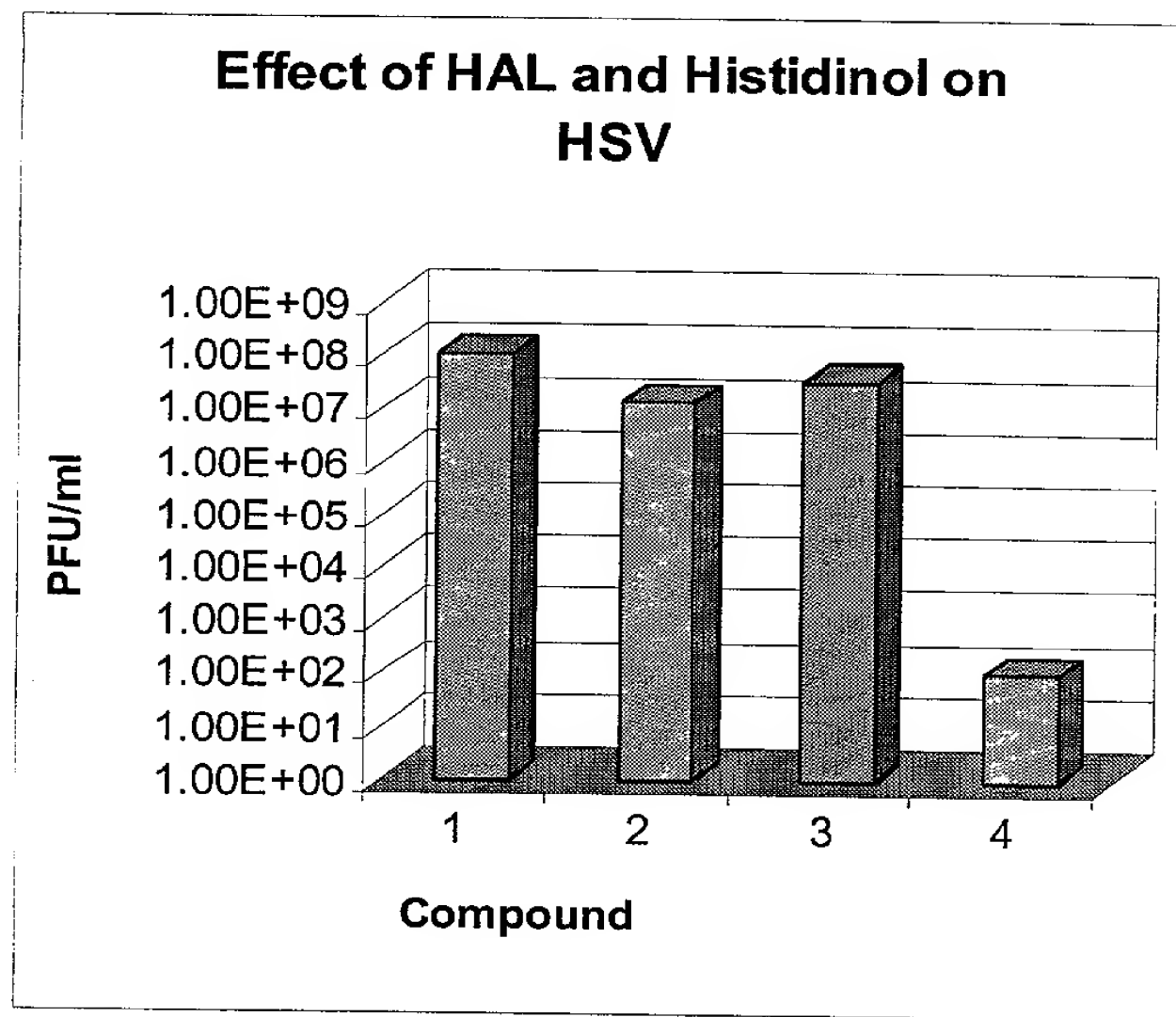




Figure 9: Effect of HAL and Histidinol on HSV.



**Figure 10:** Effectiveness of L-histidinol as a Single Agent

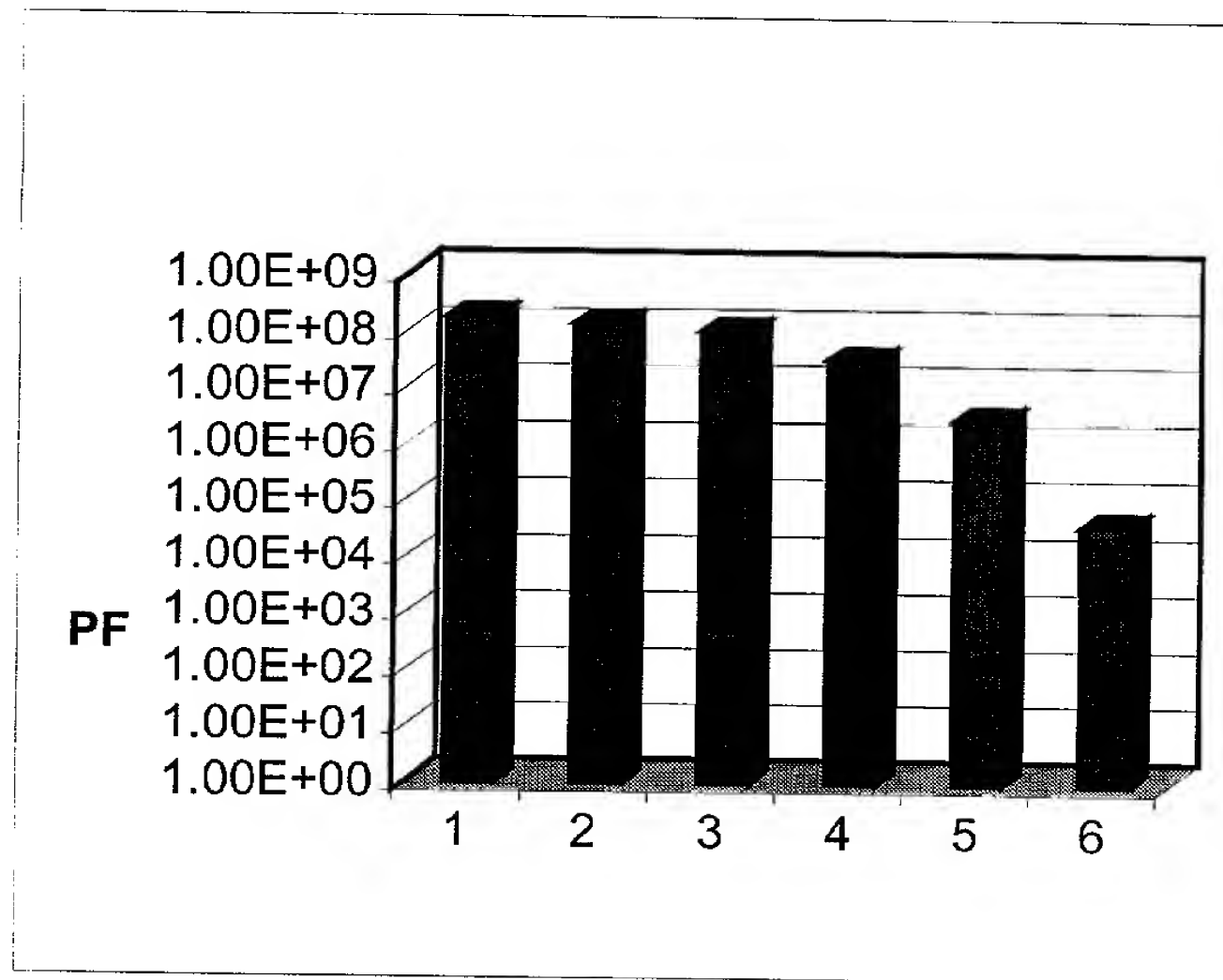


Figure 11: Effect of HAL and Histidinol on RSV.

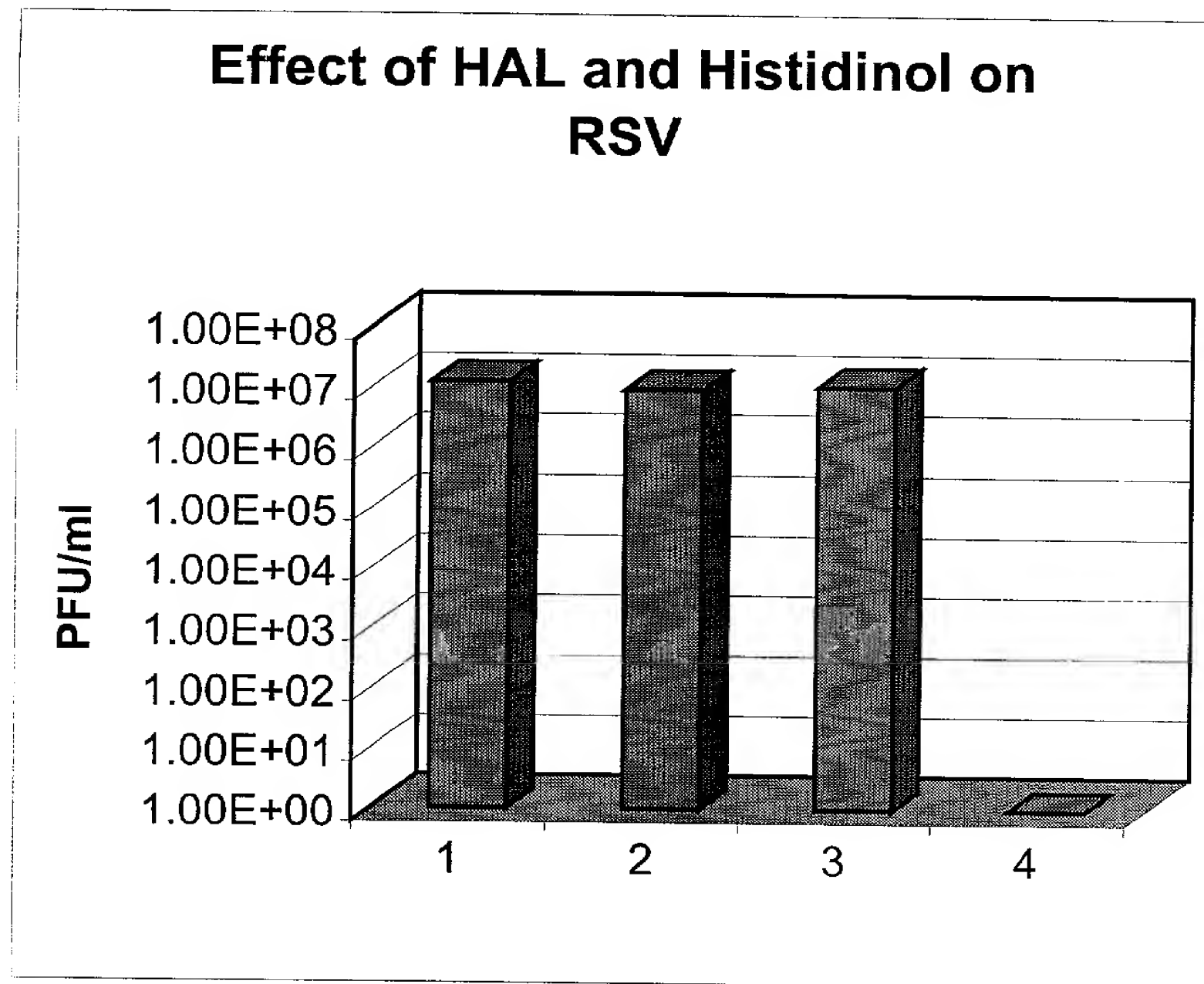




Figure 13: Histidine ammonia lyase peptide sequence pileup



**Figure 13 cont'd.**

HUTH\_PSEPU  
EDRTAYGINTGFGLLASTRIASHDLENLQ RSLVLSHAAGIGAPLDDDLVRLIMVLKINSL  
HUTH\_RHIME  
GNAPVYGIN TGFGK LASIKIDSSDVATLQ RNLILSHCCGVGQPLTEDIVRLIMALKLISL  
HUTH\_MOUSE  
ERTVVYGIT TGFGKFARTVIPANKLQ ELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL  
HUTH\_RAT  
ERTVVYGIT TGFGKFARTVIPANKLQ ELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL  
HUTH\_HUMAN  
EKTVVYGIT TGFGKFARTVIPINKLQ ELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL  
HUTH\_CAEEL  
EHRAVYGV TTGFGTFSNVTIPPEKLKKLQ LNLIRSHATGYGEPLAPNRARMLLALRINIL  
HUTH\_BACS  
DEKTIYGIN TGFGKFSDVLIQKEDSAALQ LNLILSHACGVGDPFPECVSRAMLLLRANAL  
HUTH\_STRGR  
KPEPVYGV STGFGALASRHIGTELRAQLQ RNIVRSHAAGMGRVEREVVRALMFLRLKTV  
HUTH\_CORY  
ADTPVYGISTGFGALATRHIAPEDRAKLQ RSLIRSHAAGMGEPVEREVVRALMFLRAKTL

HUTH\_PSEPU  
SRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLATMSLVLLGEGKARYKGQ  
HUTH\_RHIME  
GRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE  
HUTH\_MOUSE  
AKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS  
HUTH\_RAT  
AKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS  
HUTH\_HUMAN  
AKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEKGMWSPKS  
HUTH\_CAEEL  
AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGLLGEGKMWSPTT  
HUTH\_BACS  
LKGFSGVRAELIEQLLAFLNKRVPVPIPQQSLGASGDLAPLSHLALALIGQGEVFFEGE  
HUTH\_STRGR  
ASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDG  
HUTH\_CORY ASGRS-  
VRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHG

HUTH\_PSEPU -  
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV  
HUTH\_RHIME -  
RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST  
HUTH\_MOUSE  
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTL  
HUTH\_RAT  
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL  
HUTH\_HUMAN  
GWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL  
HUTH\_CAEEL  
GWQPADVVLKKNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALSL  
HUTH\_BACS -  
RMPAMTGLKKAGIQPVTLTLSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI  
HUTH\_STRGR  
TVRPAGELLA AHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSL  
HUTH\_CORY  
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSV

**Figure 13 cont'd.**

HUTH\_PSEPU EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----  
KVQDPYS  
HUTH\_RHIME DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---  
RVQDPYC  
HUTH\_MOUSE EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSL LDS-  
DHHPSEIAESHREFCDRVQDAYT  
HUTH\_RAT EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSL LDS-  
DHHPSEIAESHREFCDRVQDAYT  
HUTH\_HUMAN EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSL LDS-  
DHHPSEIAESHREFCDRVQDAYT  
HUTH\_CAEEL DVLKGTTTRAYDPDIHR-IRPHRGQNL SALRLRALLHS-  
EANPSQIAESHRNCTKVQDAYT  
HUTH\_BACS EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFY LSD-SGLTTSQGE-----  
LRVQDAYS  
HUTH\_STRGR EALLGTDKVLAPELHA-IRPHPGQGV SADNMSRVLAG-SGLTGHHQDDAP---  
RVQDAYS  
HUTH\_CORY EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---  
RVQDAYS

HUTH\_PSEPU  
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVF AAEGDVISGGNFHAE PVAMAADNL  
HUTH\_RHIME IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-  
SVVSGGNFHAEPVAF AADQI  
HUTH\_MOUSE  
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL  
HUTH\_RAT  
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL  
HUTH\_HUMAN  
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL  
HUTH\_CAEEL  
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL  
HUTH\_BACS  
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL  
HUTH\_STRGR VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVVL PDG-  
RVESNGNFHGAPVAYVLD FL  
HUTH\_CORY LRCSPQVTGAARDTIAHARLVATRELAAAI DN PVVLPSG-  
EVTSNGNFHGAPVAYVLD FL

HUTH\_PSEPU ALAIAEIGSLSERRISLMMDKHMS-  
QLPPFLVENGGVNSGF MIAQVTA AALASENKALSH  
HUTH\_RHIME  
ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSENKQLSH  
HUTH\_MOUSE AIGVHELAAISERRIERLCNPSLS-  
ELPAFLVAEGGLNSGF MIAHCTAAALVSESKALCH  
HUTH\_RAT AIGVHELAAISERRIERLCNPSLS-  
ELPAFLVAEGGLNSGF MIAHCTAAALVSESKALCH  
HUTH\_HUMAN AIGIHELAAISERRIERLCNPSLS-  
ELPAFLVAEGGLNSGF MIAHCTAAALVSENKALCH  
HUTH\_CAEEL AIAVAELAQMSERRLERLVNKELS-  
GLPTFLTDPDGLNSGFMTVQLCAASLVSENVLCH  
HUTH\_BACS KIAISELANIAERRIERLVNPQLN-  
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH  
HUTH\_STRGR  
AIVAADLGSICERRTRDLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV  
HUTH\_CORY  
AIAVADLGSIAERRTRDMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV

Figure 13 cont'd.

HUTH_PSEPU	PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG-LKTS
HUTH_RHIME	PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP-LTTS
HUTH_MOUSE	PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_RAT	PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_HUMAN	PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_CAEEL	PSSVDSIPTSCNQEDHVSMGGFAARKALTVEHVEAVLAMELLAACQGIEFLKP-LIST
HUTH_BACS	PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI-EHAA
HUTH_STRGR	
PASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPA	
HUTH_CORY	PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG
HUTH_PSEPU	AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTGILLPAGVLP SL---
-	
HUTH_RHIME	PELQKAAAARGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN--
HUTH_MOUSE	TPLEKVDLVR SVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_RAT	TPLEKVDLVR SVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_HUMAN	TPLEKVDLVR SVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_CAEEL	APLHKIYQLVR SVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD	
HUTH_BACS	SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI-
HUTH_STRGR	PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---
-	
HUTH_CORY	PATGAVLEVLRSKVA-GPGQDRFLSAELEAAAYDLLANG---S-VHKALEAHLPE-----
-	
HUTH_PSEPU	-----
HUTH_RHIME	-----
HUTH_MOUSE	PLSPTAFSLES LRKNSATIPESDDL----
HUTH_RAT	PLSPTAFSLES LRKNSATIPESDDL----
HUTH_HUMAN	PLSPTAFSLQFLHKKSTKIPES EDL----
HUTH_CAEEL	ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS	-----
HUTH_STRGR	-----
HUTH_CORY	-----



Figure 14

983831	1	100.0%	[	80
1 SWALL: CAC21618	66.1%	MASAPQITGLSGATADDVIAVARHEARISISPOVLEELASVRAHIDALASADTPVYIGISTGFGALATRHIAPEPRAKLQ	.	
2 SWALL: HUTH_STRGR	65.4%	---MHTVVVGTSVGTASDVLAVARAGARIELSEEAVAALAAARSVVDALAAKPDVPYGVSTGFGALATRHISPELRGRLQ	.	
3 SWALL: HUTH_DEIRA	46.8%	-MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAVEALAAARLIVDALAAKPEPVPYGVSTGFGALASRHIGTELRAQLQ	.	
4 SWALL: BAB16159	42.0%	-----MILDRDLNLEQFISVVRHGEQVELSAAARERJARARTVIEQIVEGDTPIYGVNTGFGKFENVQIDRSQLAQLQ	.	
5 SWALL: Q9KWE4	42.0%	-----VPLHHLADIYWNNGSAKLDPFDAAVLKGAARIAEIAAGNAPVYGINTEGFKLASIKIDAADLALTLQ	.	
6 SWALL: HUTH_BACSU	40.4%	-----VPLHHLADIYWNNGSAKLDPFDAAVLKGAARIAEIAAGNAPVYGINTEGFKLASIKIDAADLALTLQ	.	
7 SWALL: Q9KSQ4	42.2%	-----MVTLDGSSLTADVARVLDFEAAAASEESMERVKKSRAAVERIVRDEKTIYGINTEGFKFSDVLIQKEDSAAALQ	.	
8 SWALL: Q9HU85	41.7%	--MLHLMIKPGQLSLKQLRQVSRSPVLSLDPEAIPAIAESAQVVEQVISEGRTVYGINTEGFGLLANTKIAPQDLETLQ	.	
9 SWALL: Q9KBE6	39.3%	----MSLHLKPGQLTLADLRQAYLAPVRLSLDPSADAPIAASVACVENIIAEGRTAYGINTEGFGLLASTRISPADLEKLQ	.	
10 SWALL: HUTH_PSEPU	41.7%	---MTNLKLLDGRSLSLHDLHRIIYEGETVGASDESMKVKQSRKAVEQIIVADEKIIYGITTTGFGKFSDFIDPDDVENLQ	.	
11 SWALL: HUTH_RHIME	40.6%	---TELTLPKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTEGFGLLASTRIASHDLENLQ	.	
12 SWALL: Q9HU90	40.7%	-----LRPGSVPLSDLETIYWTGAPARLDAADFAGIAKAAARIAEIVAGNAPVYGINTEGFKLASIKIDSSDVATLQ	.	
13 SWALL: HUTH_HUMAN	39.2%	MSDLPVSVFGDGPLRWQELVAVARHGARLELSAAAARIDNARAIVCRIVANGERAYGISTGLGALCDVLLLEGEQLAELS	.	
14 SWALL: HUTH_CAEEL	38.8%	KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGITTTGFGKFA-RTVIPINKLQLQ	.	
15 SWALL: Q9HLI6	41.0%	VLAPPTKLLILDGNSPEDIVRCEKGECAIQLSMESEDRIRKARTFLEKIASEHRAVYGVTTGFTFSNVTIPPEKLLKKLQ	.	
16 SWALL: HUTH_MOUSE	38.6%	-----MIEIDGRSLRVEDVYAVAVEYDRVSI SDDTLKAVEEKHEAFLKLINSKTVYGVNTGFGSLLNVHIERDQEIQLQ	.	
17 SWALL: BAB29407	38.6%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTTGFGKFA-RTVIPANKLQLQ	.	
18 SWALL: HUTH_RAT	38.2%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTTGFGKFA-RTVIPANKLQLQ	.	
19 SWALL: AAG53586	39.8%	KYREPEKYIALDGDSTEDLVNLGKGHYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTTGFGKFA-RTVIPANKLQLQ	.	
20 SWALL: Q9KKE0	38.9%	---MNALTLPGTTLTLaQLRQVWQQLTLDESAAHEAINDSVACVEAIVAEGRYGINTEGFGLLAQTRIATHDLENLQ	.	
21 SWALL: Q9HQD5	42.2%	----MGEMISLDGPLTWREIASIAEGASLDLSGPARLRIAQAARRIVDALVERGIRGYGINTEGFGALCDVLIISRENQQALS	.	
		-----MSDTRIDAADREALQ	.	

**Figure 14, cont'd.**

Title: CLONING, OVEREXPRESSION AND  
THERAPEUTIC USE OF BIOACTIVE  
HISTIDINE AMMONIA LYASE  
Inventor(s): Joseph ROBERTS et al.  
DOCKET NO.: 078728/0106

Figure 14, cont'd.

983831	161	100.0%	1	240
1 SWALL:CAC21618	66.1%	MGE	EATDAHGDIRPVPELFAEAGLTPVELAEKEGLAVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQV	
2 SWALL:HUTH_STRGR	65.4%	MGE	GDAEGPDGTVRPAGELLAAHGIAPVLEIREKEGLALLNGTDGMLGMLVMALADLDTLYKSADITAAALTMEALLGTD	RV
3 SWALL:HUTH_DEIRA	46.8%	MGE	GEAEGPDGTVRPAGELLAAHGIAPVLEIREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAAALSLEALLGTD	DKV
4 SWALL:BAB16159	42.0%	I	GLDI-EYQGQVRPAADVLAELGLSPVOLQAKEGLALINGTQLMGSLLAIALHDAQVLLGTANLAAAMTVEARYGSHRP	
5 SWALL:Q9KWE4	42.0%	MGE	GEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSA	LV
6 SWALL:HUTH_BACSU	40.4%	MGE	GEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSA	LV
7 SWALL:Q9KSQ4	42.2%	I	QGEVF-FEGERPAMTGLKKAGIQPVTLT	SKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTIEGLQGIIDA
8 SWALL:Q9HU85	41.7%	LGE	GQAR-YNGKIIISGLEAMKIAGLEPITLAPKEGLALLNGTQASTAFALEGLFVAEDLFASATVCGAMSVEAALG	SRRP
9 SWALL:Q9KBE6	39.3%	I	ESRARH-RGEWLPAAEALAVAGLEPLTLAAKEGLALLNGTQVSTAYALRGLFEAEDLFAAATVCGGLSVEAMLG	SRAP
10 SWALL:HUTH_PSEPU	41.7%	LGE	GEVF-YKGTKT	KASFALKEEEIEPITLTAKKEGLALINGTQAMTAMGVIAYLEAEKLA
11 SWALL:HUTH_RHIME	40.6%	LGE	GKAR-YKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVL	GSRSP
12 SWALL:Q9HU90	40.7%	M	GEAFFAGERMKGDAALKA-AGLSPVTLAAKEGLALINGTQVSTALALAGLFRHRAGQAALITGALS	TD
13 SWALL:HUTH_HUMAN	39.2%	L	GIVS-YRGSVVPAAAALAAEGLATVRLGAKDGLCLVNGTPCMTGLACIALDDAQRLAQWADVIGAMSFEALRG	QLAA
14 SWALL:HUTH_CAEEL	38.8%	V	GKMWSPKSGWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAAALTLEVL	KGTTKA
15 SWALL:Q9HLI6	41.0%	L	GKMWSPTTGWQPADVVLLKNNLEPLELGPKEGLALINGTQMVVTALGAYTLERAHNIARQADVIAALS	LDV
16 SWALL:HUTH_MOUSE	38.6%	M	GKAF-FEGRIMDSARALEKAGLKPYPFKEKEGVALINGTSFMSGILSIAVMDAHDILENAIRSALLSFEAL	GGT
17 SWALL:BAB29407	38.6%	I	GKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAAALT	LEV
18 SWALL:HUTH_RAT	38.2%	I	GKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAAALT	LEV
19 SWALL:AAG53586	39.8%	L	GKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAAALT	LEV
20 SWALL:Q9KKE0	38.9%	L	GKAR-YRGEWLPAAALQKAGLAPVTLAAKEGLALLNGTQASTAFALRGLFEAEDLFASAVVCGALT	TEAV
21 SWALL:Q9HQD5	42.2%	I	GHSAMQGTERLSGADAL-ARLGLAPLRLEAKEGLSLVNGTPCATGLAALALARTERLFAWADAAAAMTYE	-NLGSQAN

Figure 14, cont'd.

983831	241	100.0%	[	320
1 SWALL:CAC21618		66.1%	FRAELHEPLRPHPGQGRSAQNMF AFLADSPIVASHREGDGRVQDAYSLRCS PQVTGAARDTIAHARLVATRELA AAI DNP	
2 SWALL:HUTH_STRGR		65.4%	LAPELHA-IRPHPGQAASAANMAAVLKSGLTGHHQDDAPRVQDAYSVRCAPQVAGAGRDTMAHAGLVAERELAAAVDNP	
3 SWALL:HUTH_DEIRA		46.8%	LAPELHA-IRPHPGQGV SADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAALVAGRELASSVDNP	
4 SWALL:BAB16159		42.0%	FQPDV-VGLRPHPGALAVAAELREFLAGSEIAPSHLTGDGKVQDAYSLRAVPQVHGATWDALAQAE RVLAVEFASVTDNP	
5 SWALL:Q9KWE4		42.0%	FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCI RCQPQVDGACLDLLASVARTLEIEANAVTDNP	
6 SWALL:HUTH_BACSU		40.4%	FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCI RCQPQVDGACLDLLASVARTLEIEANAVTDNP	
7 SWALL:Q9KSQ4		42.2%	FDEDIHLA-RGYQE QIDVAERIRFYLSDSGLTTS--QGELRVQDAYSLRCIPQVHGATWQTLYGVKEKLEIEMNAATDNP	
8 SWALL:Q9HU85		41.7%	FDPRIHR-VRGHRTQMDAATAYRHLLVSSEIGQSHSNCE-KVQDPYSLRCQPQVMGACLQQIRSAAEVLEVEANSVSDNP	
9 SWALL:Q9KBE6		39.3%	FDARIHAA-RQQRGQIDVAAAYRDLLASSEVARSHKCD-KVQDPYSLRCQPQVMGACLTQMRQAAEVLEIEANAVSDNP	
10 SWALL:HUTH_PSEPU		41.7%	FDEQIHEA-RGYVEQVDVARRMESYLQDSQLTT--RQGELRVQDAYSLRCIPQVHGATWQTLRYVKEKLEIEMNAATDNP	
11 SWALL:HUTH_RHIME		40.6%	FDARIHEA-RQQRGQIDTAACFRDLLGDSSEVSSHKNCD-KVQDPYSLRCQPQVMGACLTQLRQAAEVIGIEANAVSDNP	
12 SWALL:Q9HU90		40.7%	FHPDIQHCAAIRARSTRAAA-LRQLLTGSPIRQSHIEGDERVQDPYCI RCQPQVDGACLDLLRSVAATLTIEANAVTDNP	
13 SWALL:HUTH_HUMAN		39.2%	FDAEI-VALKPHPGMQORVAANLRALLAGSQVLENAR--GIRTQDALSI RSIPQIHGACRDQLAHARQIET-ELNSATDNP	
14 SWALL:HUTH_CAEEL		38.8%	FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHG VVNDTIAFVKNIITTELSATDNP	
15 SWALL:Q9HLI6		41.0%	YDPDIHR-IRPHRGQNLSALRLRALINPSQIAESHRNCT-KVQDAYTLRCVPQVHG VVNDTIEFVREIITTEMSATDNP	
16 SWALL:HUTH_MOUSE		38.6%	FTPWILGA-RPHLGQVAIGNRFREYLTGSDIV--KRADSVKVQDAYTLRCIPQVYGSVADVIDYVENVLSVEINSATDNP	
17 SWALL:BAB29407		38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHG VVNDTIAFVKDIITTELSATDNP	
18 SWALL:HUTH_RAT		38.2%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHG VVNDTIAFVKDIITTELSATDNP	
19 SWALL:AAG53586		39.8%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHG VVNDTIAFVKDIITTELSATDNP	
20 SWALL:Q9KKE0		38.9%	FDARIHE-VRGQRGQIDAAALFRHVLTDTSAIA SHHNCD-KVQDPYSLRCQPQVMGACLTQMRQVAEVLIVESNAVSDNP	
21 SWALL:Q9HQD5		42.2%	AFAELPLALRQSPGLS AVGEGLRDWLADSPMLAG--TAGTRTQDPLSLRAVPQVHGAARDAFGQVAEIVDRELASVTDNP	
			CAPAIHE-VRPHDGGQAVSARHIRNLTAGSEVLDHHRD CD-RVQDAYSIRCLPQVHGAVRDALDHLRAAVATELNSATDNP	

[illegible][illegible]

[ VVLP SGVTSNGNFHGAPVAYVLD FLAIAVADLGSIAERRTDRLMDPARSRDLPAFLADDPGVDSGMMIAQYTTQAGLVAE  
VVLPDGRVESNGNFHGAPVAYVLD FLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAAGVDSGLMIAQYTTQAAALVGE  
VVLPDGRVESNGNFHGAPVAYVLD FLAIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAAGVDSGLMIAQYTTQAAALVSE  
LIFPTGEVVSNGNFHGOPLAVTIDALKVAEALGSIERRTEQLLNPAIS-GLPAFLTTPNGGLNSGFMIAQYTTSAALVSE  
LVLSDNSVVSNGNFHAEPVAFADQ TALAVCEIGAI AQRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE  
LVLSDNSVVSNGNFHAEPVAFADQ TALAVCEIGAI AQRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE  
LIFNDGDV ISGNGFHGOPIAFAMDFLKIAISELANIAERRIERLVNPQLN-DLPPFLSPHPGLQSGAMIMQYAAAALVSE  
LVFADGDI ISGNGFHAEPVAMAADNLALAI AEIGLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTTAAALASE  
LVFAAGDV ISGNGFHAEPVAMAADNLALALAEIGLSERRISLMMDMHMSQ-LPPFLVANGGVNSGFMIAQVTTAAALASD  
LJFDNGQV ISGNGFHGOQIALAMDFLGIAEALANISERRIERLVNPQLN-DLPPFLSAAPGVQSGVMILQYCAASLVSE  
LVFAAGDV ISGNGFHAEPVAMAADNLALAI AEIGLSERRISLMMDKHMSQ-LPPFLVENGGVNSGFMIAQVTTAAALASE  
LVLSDNSVVSNGNFHAEPVAFADQ TALAVCEIGAI SQRRIALLVDPALSLRLPAFLAKKPGGLNSGLMIAEVTSAALMSE  
LLLGTPEVVSQANPHGESVAMAADLLAIAVAELGGVAERRDLRVNPLVS-GLPAFLVKGKPGVNSGMMITQYVAASLAGE  
MVFANGETVSGNGFHGEYPAKALDYLAIGIHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE  
LVFADREI ISGNGFHGEYPAKALD FLAIAVAELAQMSERRLERLVNKELS-GLPTFLTDPDGLNSGFMVTQOLCAASLVSE  
L-FNGEEVVSNGNFHGEPVALAADFLAIALTD LGNMVERRIARLVDTNLS-GLPPFLTDPDGLNSGYMIPQYTTAAALCNR  
MVFASGET ISGNGFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE  
MVFASGET ISGNGFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE  
MVFASGET ISGNGFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE  
LVFAANEMVFRGNFHAEPVAMAADNLALAI AEIGALSERRIALMMDKHMSQ-LPPFLVRNGGVNSGFMIAQVTTAAALASE  
AVAGSPEVHSQAHAVGAALGLAMDSLAVAEVAEVAISERRIDRLVNPLVS-GLPAFLAGDSGVSSGFMIAQYTTAAALVAE  
LVFPSGTVVSNGNFHGEVLARLGYAASALAEALAAISERRTDRLNPETOEPLFPFLAPDSGLHSGLMIPQYTTAAASLVND

Figure 14, cont'd.

983831	100.0%	[	401	480
1 SWALL: CAC21618	66.1%	NKRLAVPASVDSIPSSAMQEDHVSIGWHAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKPGPATGAVLEVLRSKVAG	.	.
2 SWALL: HUTH_STRGR	65.4%	LKRLAVPASADSI PSSAMQEDHVSIMGWSAARKLRTAVDNLARVIAVELYAAATRAIQREGLTTPAPASQAVVEAVRAAVEG	.	.
3 SWALL: HUTH_DEIRA	46.8%	MKRLAVPASADSI PSSAMQEDHVSIMGWSAARKLRTAVDNLARIVAVELYAAATRAIELRAALTTPAPASEAVVAALRAAGAG	.	.
4 SWALL: BAB16159	42.0%	NKVL SHPASVDSIPTSANQEDHVSIMGAAHAAARQLRQIVANVQTVLSIELLCAAQGLDFQQ~LRAGRGVQAAAYEYVRTFVPT	.	.
5 SWALL: Q9KWE4	42.0%	NKQMSHPASVDSIPTSANQEDHVSMAACHGARRLLAMTDNLFGLGIEALAAVQGVGVELRGPLKTSPELEKAAAALRSAPV	.	.
6 SWALL: HUTH_BACSU	40.4%	NKQMSHPASVDSIPTSANQEDHVSMAACHGARRLLAMTDNLFGLGIEALAAVQGVGVELRGPLKTSPELEKAAAALRSAPV	.	.
7 SWALL: Q9KSQ4	42.2%	NKTLAHPASVDSIPSSANQEDHVSMTGIIAARHAYQVIANTRRVIAIEAICALQAVEYRGIEHHAASYTKQLFQEMRKVVPS	.	.
8 SWALL: Q9HU85	41.7%	NKTLAHPASVDSIPSSANQEDHVSMTATFAARRLRDMGENTRGILAVEYLAQAQGLDFRAPLKSPPRIEEARQILREKVPF	.	.
9 SWALL: Q9KBE6	39.3%	NKALAHPASVDSIPSSANQEDHVSMAFNAGKRLWAMAENVRGILAVEWLGACQGLDFREGLKSSPKLEQARRLLRDKVPY	.	.
10 SWALL: HUTH_PSEPU	41.7%	NKTLAHPASVDSIPSSANQEDHVSMTGIIISRHAYQIIQNVNRNVLAIELICAMQAVDIRGREKMASTFKKILEKGREHVPY	.	.
11 SWALL: HUTH_RHIME	40.6%	NKALSHPHSVDSLPTSANQEDHVSMAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGLKTSAKLEKARQALRSEVAH	.	.
12 SWALL: Q9HU90	40.7%	NKQLSHPASVDSIPTSANQEDHVSMAACHGARRLLQMTENLFSIIIGIEALAAVQGVGIEFRAPLTTSPELQKAAAAGRVS	.	.
13 SWALL: HUTH_HUMAN	39.2%	NRQLAQPAVVDFVTSALQEDHLSLGTSAALKLGRALENLRRILAIIEYLLAAQAFEFELAPQRFQGTAAAWGILRERVPA	.	.
14 SWALL: HUTH_CAEEL	38.8%	NKALCHPSSVDSLSTSAATEDHVSIMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTTTPLEKVYDLVRSVVRP	.	.
15 SWALL: Q9HLI6	41.0%	NKVLCHPSSVDSIPTSCNQEDHVSIMGGFAARKALTVEHVEAVLAMELLAACQGIEFLKPLISTAPLHKIYQLVRS~VAP	.	.
16 SWALL: HUTH_MOUSE	38.6%	NKVLAYPSSADTIPTSANQEDHVSIMGATGSLKLEIIDNVRYIIAIEYLLGSQALEFTDK~GMSPSTRKIYEKIREKVEK	.	.
17 SWALL: BAB29407	38.6%	SKALCHPSSVDSLSTSAATEDHVSIMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRPLKTTTTPLEKVYDLVRSVVRP	.	.
18 SWALL: HUTH_RAT	38.2%	SKALCHPSSVDSLSTSAATEDHVSIMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTTTPLEKVYDLVRSVVRP	.	.
19 SWALL: AAG53586	39.8%	NKGLCHFTSVDK~PPSANQEDHVSMAAGRRRLWEMAGNTRGVLAIEWLAACQGADLRDGLTSSPLLEQARQSCGEQVAH	.	.
20 SWALL: Q9KKE0	38.9%	NRRLAAPASLDGGITSALQEDMLTHATPAAWKALSIVDNLERILAIELLAAHRPMSCSRKRARRRNAPLPFTGTYARRSP	.	.
21 SWALL: Q9HQD5	42.2%	LRSLGQP~TLDNASVSGAQEDHVSMSAGAAYNFREAVEKEAATVVGVGVELLCCGAQGREFLDPLALGAGTAAAYDLVR~EVSE	.	.

401 480



Figure 14, cont'd.

983831	481	
1 SWALL:CAC21618	100.0%	PGQDRFLSAELEAAAYDLLANGSVHKALEAHLPA
2 SWALL:HUTH_STRGR	66.1%	PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP
3 SWALL:HUTH_DEIRA	65.4%	PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP
4 SWALL:BAB16159	46.8%	LTEDRYFRPDLLRLRGELVSGRVAQAADTQAPA
5 SWALL:Q9KWE4	42.0%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
6 SWALL:HUTH_BACSU	42.0%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
7 SWALL:Q9KSQ4	40.4%	IQQDRVFSYDIERLTDWLKKESLIPDHQNKELR
8 SWALL:Q9HU85	42.2%	YKDRYFAPDIEKANALL-Q LAVHNRLMPDQLL
9 SWALL:Q9KBE6	41.7%	YQEDRFFAPDIEAASQILASGCINALLPARLLP
10 SWALL:HUTH_PSEPU	39.3%	IDQDRMFAKDIERA AKWLKDGSWDFTKMREKER
11 SWALL:HUTH_RHIME	41.7%	YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS
12 SWALL:Q9HU90	40.6%	IEEDRYMADDLKAAGDLVASGRLAAAVSAGLPK
13 SWALL:HUTH_HUMAN	40.7%	YDTRWLAPDIAASAAIIGERKSIARLAASIGD
14 SWALL:HUTH_CAEEL	39.2%	WIKDRFMAPDIEAAHRLLLLEQKVWEVAAPYIEK
15 SWALL:Q9HLI6	38.8%	PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET
16 SWALL:HUTH_MOUSE	41.0%	LDHDRPPSFDIETIRKMMDKKEFISALP-----
17 SWALL:BAB29407	38.6%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
18 SWALL:HUTH_RAT	38.6%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
19 SWALL:AAG53586	38.2%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
20 SWALL:Q9KKE0	39.8%	YDDDRFFAPDIEAAISLNLKGSVLGLLPAFL--
21 SWALL:Q9HQD5	38.9%	PIATIVR-----
	42.2%	PAGDRALADDMAAVGDLVRAGLVEDAVARALDA

Figure 14, cont'd.

KEY:

983831	:	HAL
1	CAC21618	: Streptomyces coelicolor
2	HUTH_STRGR	: Streptomyces griseus
3	HUTH_DEIRA	: Deinococcus radiodurans
4	BAB16159	: Agrobacterium rhizogenes
5	Q9KWE4	: Agrobacterium rhizogenes
6	HUTH_BACSU	: Bacillus subtilis
7	Q9KSQ4	: Vibrio cholerae
8	Q9HU85	: Pseudomonas aeruginosa
9	Q9KBE6	: Bacillus halodurans
10	HUTH_PSEPU	: Pseudomonas putida
11	HUTH_RHIME	: Rhizobium meliloti
12	Q9HU90	: Pseudomonas aeruginosa
13	HUTH_HUMAN	: Human
14	HUTH_CAEEL	: Caenorhabditis elegans
15	Q9HLI6	: Thermoplasma acidophilum
16	HUTH_MOUSE	: Mouse
17	BAB29407	: Mus musculus (Mouse)
18	HUTH_RAT	: Rat
18	AAG53586	: uncultured bacterium pCosAS1
20	Q9KKE0	: Rhizobium meliloti
21	Q9HQD5	: Halobacterium sp



Table 15

Figure 15

STRG	6	VVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL	
"HAL"	7	ITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISGTFGAL	* * * * *
STRG,	66	ASRHIGTELRAQLQRNIVRSHAAAGMGPVEREVVRALMFLRLKTVASGHTGVRPEVAQTM	* * * * *
HAL	67	ATRHIAPEDRAKLQRSLIRSHAAAGMGPVEREVVRALMFLRAKTLASGRTGVRPVVLETM	* * * * *
STRG	126	ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDGTVRPAGELLAAHGIA	* * * * *
HAL	127	VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT	* * * * *
STRG	186	PVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAAALSLEALLGTDKVLAPELH	* * * * *
HAL	187	PVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSVEAQIGTDQVFRANELH	* * * * *
STRG	246	A-IRPHPGQGSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA	* * * * *
HAL	247	EPLRPHPGQGRSAQNMFADSPIVASHREGDGRVQDAYSLRCSPPQVTGAARDTIAHAR	* * * * *
STRG	305	LVAGRELAASSVDNPVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLD	* * * * *
HAL	307	LVATRELAADNPVLPSPGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLD	* * * * *

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STRG      365 KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSI PSSAMQEDHVS MG
HAL        367 PARSRDLP AFLADDPGVDS GMMIAQTQAGLVAENKRLAVPASVD SI PSSAMQEDHVSLG
          **   **   **** * * * * * * * * * * * * * * * * * * * * * * *
STRG      425 WSAARKLR TAVDN LARI VAVEL YAA TRAI ELRAA EGLTPAPASE AVVAAL RAAGAEGP GP
HAL        427 WHAARKLR TSVAN LRRI LAVEM LIAGR ALDLRAP --LKPGPATGA VLEVLRSKVA -GPGQ
          *   ***** * * * * * * * * * * * * * * * * * * * * * * *
STRG      485 DRFLAPD LAAADTFVREG RLVA AVE
HAL        484 DRFLS AELEA AYDLLANG SVHKALE
          ***** * * * * * * * * * * * * * * * * * * * * * * *

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STRG      365 KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSI PSSAMQEDHVS MG
HAL        367 PARSRDLP AFLADDPGVDS GMMIAQTQAGLVAENKRLAVPASVD SI PSSAMQEDHVSLG
          **   **   **** * * * * * * * * * * * * * * * * * * * * * * *
STRG      425 WSAARKLR TAVDN LARI VAVEL YAA TRAI ELRAA EGLTPAPASE AVVAAL RAAGAEGP GP
HAL        427 WHAARKLR TSVAN LRRI LAVEM LIAGR ALDLRAP --LKPGPATGA VLEVLRSKVA -GPGQ
          *   ***** * * * * * * * * * * * * * * * * * * * * * * *
STRG      485 DRFLAPD LAAADTFVREG RLVA AVE
HAL        484 DRFLS AELEA AYDLLANG SVHKALE
          ***** * * * * * * * * * * * * * * * * * * * * * * *

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